IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

SAVERIO C. FALCO ET AL CASE NO.: BB1193DIV

SERIAL NO.: UNKNOWN GROUP ART UNIT: UNKNOWN

FILED: CONCURRENTLY HEREWITH EXAMINER: UNKNOWN

FOR: PLANT AMINOACYL-TRNA SYNTHETASE

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents Washington, DC 20231

Sir:

Prior to examination on the merits, please amend the above-referenced application as follows:

IN THE CLAIMS

Please cancel claims 1-30.

Please add the following new claims:

- 31. An isolated polynucleotide comprising:
- (a) a nucleotide sequence encoding an lysyl-tRNA synthetase, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:10 or SEQ ID NO:14 have at least 80% identity based on the Clustal alignment method, or
 - (b) the complement of the nucleotide sequence.
- 32. The polynucleotide of claim 31, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:10 or SEQ ID NO:14 have 85% identity based on the Clustal alignment method.
- 33. The polynucleotide of claim 31, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:10 or SEQ ID NO:14 have 90% identity based on the Clustal alignment method.
- 34. The polynucleotide of claim 31, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:10 or SEQ ID NO:14 have 95% identity based on the Clustal alignment method.
- 35. The polynucleotide of claim 31 comprising the nucleotide sequence of SEQ ID NO:9 or SEQ ID NO:13.
- 36. The polynucleotide of claim 31, wherein the synthetase comprises the amino acid sequence of SEQ ID NO:10 or SEQ ID NO:14.
- 37. A chimeric gene comprising the polynucleotide of claim 31 operably linked to a regulatory sequence.
 - 38. A vector comprising the polynucleotide of claim 31.

- 39. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 31.
 - 40. A cell comprising the chimeric gene of claim 37.
- 41. A method for producing a plant comprising transforming a plant cell with the chimeric gene of claim 31 and regenerating a plant from the transformed plant cell.
 - 42. A plant comprising the chimeric gene of claim 37.
 - 43. A seed comprising the chimeric gene of claim 37.
 - 44. An isolated polynucleotide comprising:
- (a) a nucleotide sequence encoding an lysyl-tRNA synthetase, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:16 have at least 90% identity based on the Clustal alignment method, or
 - (b) the complement of the nucleotide sequence.
- 45. The polynucleotide of claim 44, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:16 have 95% identity based on the Clustal alignment method.
- 46. The polynucleotide of claim 44 comprising the nucleotide sequence of SEQ ID NO:15.
- 47. The polynucleotide of claim 44, wherein the synthetase comprises the amino acid sequence of SEQ ID NO:16.
- 48. A chimeric gene comprising the polynucleotide of claim 44 operably linked to a regulatory sequence.
 - 49. A vector comprising the polynucleotide of claim 44.
- 50. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 44.
 - 51. A cell comprising the chimeric gene of claim 48.
- 52. A method for producing a plant comprising transforming a plant cell with the chimeric gene of claim 44 and regenerating a plant from the transformed plant cell.
 - 53. A plant comprising the chimeric gene of claim 48.
 - 54. A seed comprising the chimeric gene of claim 48.
 - 55. An isolated polynucleotide comprising:
- (a) a nucleotide sequence encoding an lysyl-tRNA synthetase, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method, or
 - (b) the complement of the nucleotide sequence.
- 56. The polynucleotide of claim 55, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:12 have 90% identity based on the Clustal alignment method.

- 57. The polynucleotide of claim 55, wherein the amino acid sequence of the synthetase and the amino acid sequence of SEQ ID NO:12 have 95% identity based on the Clustal alignment method.
- 58. The polynucleotide of claim 55 comprising the nucleotide sequence of SEQ ID NO:11.
- 59. The polynucleotide of claim 55, wherein the synthetase comprises the amino acid sequence of SEQ ID NO:12.
- 60. A chimeric gene comprising the polynucleotide of claim 55 operably linked to a regulatory sequence.
 - 61. A vector comprising the polynucleotide of claim 55.
- 62. A method for transforming a cell comprising transforming a cell with the polynucleotide of claim 55.
 - 63. A cell comprising the chimeric gene of claim 60.
- 64. A method for producing a plant comprising transforming a plant cell with the chimeric gene of claim 55 and regenerating a plant from the transformed plant cell.
 - 65. A plant comprising the chimeric gene of claim 60.
 - 66. A seed comprising the chimeric gene of claim 60.

REMARKS

Claims 1-30 have been cancelled, and claims 31-66 have been added. Claims 31-66 are pending.

Support for the sequence identities recited in the claims is found on page 6, first full paragraph of the specification. Support for claims 41-43, 52-54, and 64-66 is found in Examples 7 and 8, pages 22 through 25 of the specification.

Please charge any necessary fee to Deposit Account 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,

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Dated: 24 2001